

SEQUENCE LISTING

<110> Liang, Yanbin
Woodward, David F.

<120> Human Prostaglandin DP Receptor Variants
and Methods of Using Same

<130> 66872-029 (AR5747)

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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ggc aac tcg gcg gtg atg ggc ggg gtg ctc ttc agc acc ggc ctc ctg	96
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35 40 45	

tgc tcg cgg cgt cca ctg cgc ccg ctg ccc tcg gtc ttc tac atg ctg	192
Cys Ser Arg Arg Pro Leu Arg Pro Leu Pro Ser Val Phe Tyr Met Leu	
50 55 60	

gtg tgt ggc ctg acg gtc acc gac ttg ctg ggc aag tgc ctc cta agc	240
Val Cys Gly Leu Thr Val Thr Asp Leu Leu Gly Lys Cys Leu Leu Ser	
65 70 75 80	

ccg gtg gtg ctg gct gcc tac gct cag aac cgg agt ctg cgg gtg ctt	288
Pro Val Val Leu Ala Ala Tyr Ala Gln Asn Arg Ser Leu Arg Val Leu	
85 90 95	

gcg ccc gca ttg gac aac tcg ttg tgc caa gcc ttc gcc ttc ttc atg	336
Ala Pro Ala Leu Asp Asn Ser Leu Cys Gln Ala Phe Ala Phe Phe Met	
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gag tgc tgg ctc tcc cta ggg cac cct ttc ttc tac cga cgg cac atc Glu Cys Trp Leu Ser Leu Gly His Pro Phe Phe Tyr Arg Arg His Ile 130 135 140	432
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tcg ctg tcg gtg ctg ggg tac tct gtg ctc tac tcc agc ctc atg gcg Ser Leu Ser Val Leu Gly Tyr Ser Val Leu Tyr Ser Ser Leu Met Ala 195 200 205	624
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ctc tat gcg atg cac cgg cgg ctg cag cgg cac ccg cgc tcc tgc acc Leu Tyr Ala Met His Arg Arg Leu Gln Arg His Pro Arg Ser Cys Thr 225 230 235 240	720
agg gac tgt gcc gag ccg cgc gcg gac ggg agg gaa gcg tcc cct cag Arg Asp Cys Ala Glu Pro Arg Ala Asp Gly Arg Glu Ala Ser Pro Gln 245 250 255	768
ccc ctg gag gag ctg gat cac ctc ctg ctg ctg gcg ctg atg acc gtg Pro Leu Glu Glu Leu Asp His Leu Leu Leu Leu Ala Leu Met Thr Val 260 265 270	816
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ccc gcc aag aca cct ggg agt agg tgaggcttga ggaaacattt tcagtgtgc Pro Ala Lys Thr Pro Gly Ser Arg 290 295	918
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<213> Homo sapiens

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<220>

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<222> (1)...(1080)

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ggc aac tcg gcg gtg atg ggc ggg gtg ctc ttc agc acc ggc ctc ctg	96
Gly Asn Ser Ala Val Met Gly Gly Val Leu Phe Ser Thr Gly Leu Leu	
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ggc aac ctg ctg gcc ctg ggg ctg ctg gcg cgc tcg ggg ctg ggg tgg	144
Gly Asn Leu Leu Ala Leu Gly Leu Leu Ala Arg Ser Gly Leu Gly Trp	
35 40 45	
tgc tcg cgg cgt cca ctg cgc ccg ctg ccc tcg gtc ttc tac atg ctg	192
Cys Ser Arg Arg Pro Leu Arg Pro Leu Pro Ser Val Phe Tyr Met Leu	
50 55 60	
gtg tgt ggc ctg acg gtc acc gac ttg ctg ggc aag tgc ctc cta agc	240
Val Cys Gly Leu Thr Val Thr Asp Leu Leu Gly Lys Cys Leu Leu Ser	
65 70 75 80	
ccg gtg gtg ctg gct gcc tac gct cag aac cgg agt ctg cgg gtg ctt	288
Pro Val Val Leu Ala Ala Tyr Ala Gln Asn Arg Ser Leu Arg Val Leu	
85 90 95	
gcg ccc gca ttg gac aac tcg ttg tgc caa gcc ttc gcc ttc ttc atg	336
Ala Pro Ala Leu Asp Asn Ser Leu Cys Gln Ala Phe Ala Phe Phe Met	
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tac tgc ccc ggc acc tgg tgc ttt atc cag atg gtc cac gag gag ggc	576
Tyr Cys Pro Gly Thr Trp Cys Phe Ile Gln Met Val His Glu Glu Gly	
180 185 190	
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Trp	Ile	Phe	Ile	Ile	Phe	Arg	Ser	Pro	Val	Phe	Arg	Ile	Phe	Phe	His	
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Thr	Asn	Met	Glu	Ser	Ser	Leu	*									
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Cys	Ser	Arg	Arg	Pro	Leu	Arg	Pro	Leu	Pro	Ser	Val	Phe	Tyr	Met	Leu
	50		55		60										
Val	Cys	Gly	Leu	Thr	Val	Thr	Asp	Leu	Leu	Gly	Lys	Cys	Leu	Leu	Ser
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Pro	Val	Val	Leu	Ala	Ala	Tyr	Ala	Gln	Asn	Arg	Ser	Leu	Arg	Val	Leu
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Ala	Pro	Ala	Leu	Asp	Asn	Ser	Leu	Cys	Gln	Ala	Phe	Ala	Phe	Phe	Met
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Ser	Phe	Phe	Gly	Leu	Ser	Ser	Thr	Leu	Gln	Leu	Leu	Ala	Met	Ala	Leu
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Glu	Cys	Trp	Leu	Ser	Leu	Gly	His	Pro	Phe	Phe	Tyr	Arg	Arg	His	Ile
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Thr	Leu	Arg	Leu	Gly	Ala	Leu	Val	Ala	Pro	Val	Val	Ser	Ala	Phe	Ser
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Tyr	Cys	Pro	Gly	Thr	Trp	Cys	Phe	Ile	Gln	Met	Val	His	Glu	Glu	Gly
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Ser	Leu	Ser	Val	Leu	Gly	Tyr	Ser	Val	Leu	Tyr	Ser	Ser	Leu	Met	Ala
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Leu	Leu	Val	Leu	Ala	Thr	Val	Leu	Cys	Asn	Leu	Gly	Ala	Met	Arg	Asn
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Leu	Tyr	Ala	Met	His	Arg	Arg	Leu	Gln	Arg	His	Pro	Arg	Ser	Cys	Thr
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Arg	Asp	Cys	Ala	Glu	Pro	Arg	Ala	Asp	Gly	Arg	Glu	Ala	Ser	Pro	Gln
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Pro	Leu	Glu	Glu	Leu	Asp	His	Leu	Leu	Leu	Leu	Ala	Leu	Met	Thr	Val
			260		265										270
Leu	Phe	Thr	Met	Cys	Ser	Leu	Pro	Val	Ile	Tyr	Arg	Ala	Tyr	Tyr	Gly
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Ala	Phe	Lys	Asp	Val	Lys	Glu	Lys	Asn	Arg	Thr	Ser	Glu	Glu	Ala	Glu
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Asp	Leu	Arg	Ala	Leu	Arg	Phe	Leu	Ser	Val	Ile	Ser	Ile	Val	Asp	Pro
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Trp	Ile	Phe	Ile	Ile	Phe	Arg	Ser	Pro	Val	Phe	Arg	Ile	Phe	Phe	His
			325		330										335
Lys	Ile	Phe	Ile	Arg	Pro	Leu	Arg	Tyr	Arg	Ser	Arg	Cys	Ser	Asn	Ser
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